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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/783,931

DATE: 12/05/2001
TIME: 11:51:31

Input Set : A:\7326-122
Output Set: N:\CRF3\11212001\I783931.raw

ENTERED

SEQUENCE LISTING

```
C--> 5  (1) GENERAL INFORMATION:
     7       (i) APPLICANT: Ish-Horowicz, David
     8                      Henrique, Domingos Manuel Pinto
     9                      Lewis, Julian Hart
    10                      Artavanis-Tsakonas, Spyridon
    11                      Gray, Grace
C--> 13      (ii) TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
    14                                 AND FRAGMENTS
    16     (iii) NUMBER OF SEQUENCES: 94
    18      (iv) CORRESPONDENCE ADDRESS:
    19           (A) ADDRESSEE: Pennie & Edmonds LLP
    20           (B) STREET: 1155 Avenue of the Americas
    21           (C) CITY: New York
    22           (D) STATE: NY
    23           (E) COUNTRY: USA
    24           (F) ZIP: 10036/2711
    26       (v) COMPUTER READABLE FORM:
    27           (A) MEDIUM TYPE: Diskette
    28           (B) COMPUTER: IBM Compatible
    29           (C) OPERATING SYSTEM: DOS
    30           (D) SOFTWARE: FastSEQ Version 2.0
    32      (vi) CURRENT APPLICATION DATA:
C--> 33           (A) APPLICATION NUMBER: US/09/783,931
C--> 34           (B) FILING DATE: 15-Feb-2001
    40           (C) CLASSIFICATION:
    37     (vii) PRIOR APPLICATION DATA:
    38           (A) APPLICATION NUMBER: 08/981,392
    39           (B) FILING DATE: 22-DEC-1997
    42    (viii) ATTORNEY/AGENT INFORMATION:
    43           (A) NAME: Antler, Adriane M.
    44           (B) REGISTRATION NUMBER: 32,605
    45           (C) REFERENCE/DOCKET NUMBER: 7326-122
    47      (ix) TELECOMMUNICATION INFORMATION:
    48           (A) TELEPHONE: 212-790-9090
    49           (B) TELEFAX: 212-869-8864
    50           (C) TELEX: 66141 PENNIE
    53  (2) INFORMATION FOR SEQ ID NO: 1:
    55       (i) SEQUENCE CHARACTERISTICS:
    56           (A) LENGTH: 2508 base pairs
    57           (B) TYPE: nucleic acid
    58           (C) STRANDEDNESS: single
    59           (D) TOPOLOGY: linear
W--> 61      (ii) MOLECULE TYPE: DNA
    62      (ix) FEATURE:
    64           (A) NAME/KEY: Coding Sequence
    65           (B) LOCATION: 277...2460
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```
66        (D) OTHER INFORMATION:
69     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71   GAATTCGGCA CGAGGTTTTT TTTTTTTTTT TTCCCCTCTT TTCTTTCTTT TCCTTTTGCC      60
72   ATCCGAAAGA GCTGTCAGCC GCCGCCGGGC TGCACCTAAA GGCGTCGGTA GGGGGATAAC     120
73   AGTCAGAGAC CCTCCTGAAA GCAGGAGACG GGACGGTACC CCTCCGGCTC TGCGGGGCGG     180
74   CTGCGGCCCC TCCGTTCTTT CCCCCTCCCC GAGAGACACT CTTCCTTTCC CCCCACGAAG     240
75   ACACAGGGGC AGGAACGCGA GCGCTGCCCC TCCGCC ATG GGA GGC CGC TTC CTG      294
76                                          Met Gly Gly Arg Phe Leu
77                                           1                   5
79   CTG ACG CTC GCC CTC CTC TCG GCG CTG CTG TGC CGC TGC CAG GTT GAC      342
80   Leu Thr Leu Ala Leu Leu Ser Ala Leu Leu Cys Arg Cys Gln Val Asp
81                10                  15                  20
83   GGC TCC GGG GTG TTC GAG CTG AAG CTG CAG GAG TTT GTC AAC AAG AAG      390
84   Gly Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys
85           25                  30                  35
87   GGG CTG CTC AGC AAC CGC AAC TGC TGC CGG GGG GGC GGC CCC GGA GGC      438
88   Gly Leu Leu Ser Asn Arg Asn Cys Cys Arg Gly Gly Gly Pro Gly Gly
89       40                  45                  50
91   GCC GGG CAG CAG CAG TGC GAC TGC AAG ACC TTC TTC CGC GTC TGC CTG      486
92   Ala Gly Gln Gln Gln Cys Asp Cys Lys Thr Phe Phe Arg Val Cys Leu
93   55                  60                  65                  70
95   AAG CAC TAC CAG GCC AGC GTC TCC CCC GAG CCG CCC TGC ACC TAC GGC      534
96   Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly
97                   75                  80                  85
99   AGC GCC ATC ACC CCC GTC CTC GGC GCC AAC TCC TTC AGC GTC CCC GAC      582
100  Ser Ala Ile Thr Pro Val Leu Gly Ala Asn Ser Phe Ser Val Pro Asp
101                  90                  95                 100
103  GGC GCG GGC GGC GCC GAC CCC GCC TTC AGC AAC CCC ATC CGC TTC CCC      630
104  Gly Ala Gly Gly Ala Asp Pro Ala Phe Ser Asn Pro Ile Arg Phe Pro
105                 105                 110                 115
107  TTC GGC TTC ACC TGG CCC GGC ACC TTC TCG CTC ATC ATC GAG GCT CTG      678
108  Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu
109      120                 125                 130
111  CAC ACC GAC TCC CCC GAC GAC CTC ACC ACA GAA AAC CCC GAG CGC CTC      726
112  His Thr Asp Ser Pro Asp Asp Leu Thr Thr Glu Asn Pro Glu Arg Leu
113  135                 140                 145                 150
115  ATC AGC CGC CTG GCC ACC CAG AGG CAC CTG GCG GTG GGC GAG GAG TGG      774
116  Ile Ser Arg Leu Ala Thr Gln Arg His Leu Ala Val Gly Glu Glu Trp
117                 155                 160                 165
119  TCC CAG GAC CTG CAC AGC AGC GGC CGC ACC GAC CTC AAG TAC TCC TAT      822
120  Ser Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr
121                 170                 175                 180
123  CGC TTT GTG TGT GAT GAG CAC TAC TAC GGG GAA GGC TGC TCT GTC TTC      870
124  Arg Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe
125                 185                 190                 195
127  TGC CGG CCC CGT GAC GAC CGC TTC GGT CAC TTC ACC TGT GGA GAG CGT      918
128  Cys Arg Pro Arg Asp Asp Arg Phe Gly His Phe Thr Cys Gly Glu Arg
129      200                 205                 210
131  GGC GAG AAG GTC TGC AAC CCA GGC TGG AAG GGC CAG TAC TGC ACT GAG      966
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132   Gly Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Gln Tyr Cys Thr Glu
133   215                     220                 225                 230
135   CCG ATT TGC TTG CCT GGG TGT GAC GAG CAG CAC GGC TTC TGC GAC AAA      1014
136   Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys
137                       235                 240                 245
139   CCT GGG GAA TGC AAG TGC AGA GTG GGT TGG CAG GGG CGG TAC TGT GAC      1062
140   Pro Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp
141                       250                 255                 260
143   GAG TGC ATC CGA TAC CCA GGC TGC CTG CAC GGT ACC TGT CAG CAG CCA      1110
144   Glu Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro
145                   265                 270                 275
147   TGG CAG TGC AAC TGC CAG GAA GGC TGG GGC GGC CTT TTC TGC AAC CAG      1158
148   Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln
149             280                 285                 290
151   GAC CTG AAC TAC TGC ACT CAC CAC AAG CCA TGC AAG AAT GGT GCC ACA      1206
152   Asp Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr
153   295                     300                 305                 310
155   TGC ACC AAC ACC GGT CAG GGG AGC TAC ACT TGT TCT TGC CGA CCT GGG      1254
156   Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly
157                       315                 320                 325
159   TAC ACA GGC TCC AGC TGC GAG ATT GAA ATC AAC GAA TGT GAT GCC AAC      1302
160   Tyr Thr Gly Ser Ser Cys Glu Ile Glu Ile Asn Glu Cys Asp Ala Asn
161                   330                 335                 340
163   CCT TGC AAG AAT GGT GGA AGC TGC ACG GAT CTC GAG AAC AGC TAT TCC      1350
164   Pro Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser
165             345                 350                 355
167   TGT ACC TGC CCC CCA GGC TTC TAT GGT AAA AAC TGT GAG CTG AGT GCA      1398
168   Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys Asn Cys Glu Leu Ser Ala
169   360                     365                 370
171   ATG ACT TGT GCT GAT GGA CCG TGC TTC AAT GGA GGG CGA TGC ACT GAC      1446
172   Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Thr Asp
173   375                     380                 385                 390
175   AAC CCT GAT GGT GGA TAC AGC TGC CGC TGC CCA CTG GGT TAT TCT GGG      1494
176   Asn Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Leu Gly Tyr Ser Gly
177                       395                 400                 405
179   TTC AAC TGT GAA AAG AAA ATC GAT TAC TGC AGT TCC AGC CCT TGT GCT      1542
180   Phe Asn Cys Glu Lys Lys Ile Asp Tyr Cys Ser Ser Ser Pro Cys Ala
181             410                 415                 420
183   AAT GGA GCC CAG TGC GTT GAC CTG GGG AAC TCC TAC ATA TGC CAG TGC      1590
184   Asn Gly Ala Gln Cys Val Asp Leu Gly Asn Ser Tyr Ile Cys Gln Cys
185                   425                 430                 435
187   CAG GCT GGC TTC ACT GGC AGG CAC TGT GAC GAC AAC GTG GAC GAT TGC      1638
188   Gln Ala Gly Phe Thr Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys
189       440                 445                 450
191   GCC TCC TTC CCC TGC GTC AAT GGA GGG ACC TGT CAG GAT GGG GTC AAC      1686
192   Ala Ser Phe Pro Cys Val Asn Gly Gly Thr Cys Gln Asp Gly Val Asn
193   455                     460                 465                 470
195   GAC TAC TCC TGC ACC TGC CCC CCG GGA TAC AAC GGG AAG AAC TGC AGC      1734
196   Asp Tyr Ser Cys Thr Cys Pro Pro Gly Tyr Asn Gly Lys Asn Cys Ser
```

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```
197                  475                 480                485
199     ACG CCG GTG AGC AGA TGC GAG CAC AAC CCC TGC CAC AAT GGG GCC ACC      1782
200     Thr Pro Val Ser Arg Cys Glu His Asn Pro Cys His Asn Gly Ala Thr
201                  490                 495                500
203     TGC CAC GAG AGA AGC AAC CGC TAC GTG TGC GAG TGC GCT CGG GGC TAC      1830
204     Cys His Glu Arg Ser Asn Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr
205                  505                 510                515
207     GGC GGC CTC AAC TGC CAG TTC CTG CTC CCC GAG CCA CCT CAG GGG CCG      1878
208     Gly Gly Leu Asn Cys Gln Phe Leu Leu Pro Glu Pro Pro Gln Gly Pro
209                  520                 525                530
211     GTC ATC GTT GAC TTC ACC GAG AAG TAC ACA GAG GGC CAG AAC AGC CAG      1926
212     Val Ile Val Asp Phe Thr Glu Lys Tyr Thr Glu Gly Gln Asn Ser Gln
213     535                  540                 545                550
215     TTT CCC TGG ATC GCA GTG TGC GCC GGG ATT ATT CTG GTC CTC ATG CTG      1974
216     Phe Pro Trp Ile Ala Val Cys Ala Gly Ile Ile Leu Val Leu Met Leu
217                  555                 560                565
219     CTG CTG GGT TGC GCC GCC ATC GTC GTC TGC GTC AGG CTG AAG GTG CAG      2022
220     Leu Leu Gly Cys Ala Ala Ile Val Val Cys Val Arg Leu Lys Val Gln
221                  570                 575                580
223     AAG AGG CAC CAC CAG CCC GAG GCC TGC AGG AGT GAA ACG GAG ACC ATG      2070
224     Lys Arg His His Gln Pro Glu Ala Cys Arg Ser Glu Thr Glu Thr Met
225                  585                 590                595
227     AAC AAC CTG GCG AAC TGC CAG CGC GAG AAG GAC ATC TCC ATC AGC GTC      2118
228     Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Ile Ser Val
229     600                  605                610
231     ATC GGT GCC ACT CAG ATT AAA AAC ACA AAT AAG AAA GTA GAC TTT CAC      2166
232     Ile Gly Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Val Asp Phe His
233     615                  620                 625                630
235     AGC GAT AAC TCC GAT AAA AAC GGC TAC AAA GTT AGA TAC CCA TCA GTG      2214
236     Ser Asp Asn Ser Asp Lys Asn Gly Tyr Lys Val Arg Tyr Pro Ser Val
237                  635                 640                645
239     GAT TAC AAT TTG GTG CAT GAA CTC AAG AAT GAG GAC TCT GTG AAA GAG      2262
240     Asp Tyr Asn Leu Val His Glu Leu Lys Asn Glu Asp Ser Val Lys Glu
241                  650                 655                660
243     GAG CAT GGC AAA TGC GAA GCC AAG TGT GAA ACG TAT GAT TCA GAG GCA      2310
244     Glu His Gly Lys Cys Glu Ala Lys Cys Glu Thr Tyr Asp Ser Glu Ala
245                  665                 670                675
247     GAA GAG AAA AGC GCA GTA CAG CTA AAA AGT AGT GAC ACT TCT GAA AGA      2358
248     Glu Glu Lys Ser Ala Val Gln Leu Lys Ser Ser Asp Thr Ser Glu Arg
249     680                  685                690
251     AAA CGG CCA GAT TCA GTA TAT TCC ACT TCA AAG GAC ACA AAG TAC CAG      2406
252     Lys Arg Pro Asp Ser Val Tyr Ser Thr Ser Lys Asp Thr Lys Tyr Gln
253     695                  700                 705                710
255     TCG GTG TAC GTC ATA TCA GAA GAG AAA GAT GAG TGC ATC ATA GCA ACT      2454
256     Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Ile Ile Ala Thr
257                  715                 720                725
259     GAG GTG TAAAACAGAC GTGACGTGGC AAAGCTTATC GATACCGTCA TCAAGCTT        2508
260     Glu Val
264 (2) INFORMATION FOR SEQ ID NO: 2:
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```
266        (i) SEQUENCE CHARACTERISTICS:
267            (A) LENGTH: 728 amino acids
268            (B) TYPE: amino acid
269            (C) STRANDEDNESS:
270            (D) TOPOLOGY: unknown
272       (ii) MOLECULE TYPE: protein
274       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
276    Met Gly Gly Arg Phe Leu Leu Thr Leu Ala Leu Leu Ser Ala Leu Leu
277     1               5              10              15
278    Cys Arg Cys Gln Val Asp Gly Ser Gly Val Phe Glu Leu Lys Leu Gln
279            20              25              30
280    Glu Phe Val Asn Lys Lys Gly Leu Leu Ser Asn Arg Asn Cys Cys Arg
281        35              40              45
282    Gly Gly Gly Pro Gly Gly Ala Gly Gln Gln Gln Cys Asp Cys Lys Thr
283        50              55              60
284    Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala Ser Val Ser Pro Glu
285    65              70              75              80
286    Pro Pro Cys Thr Tyr Gly Ser Ala Ile Thr Pro Val Leu Gly Ala Asn
287                85              90              95
288    Ser Phe Ser Val Pro Asp Gly Ala Gly Gly Ala Asp Pro Ala Phe Ser
289            100             105             110
290    Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser
291        115             120             125
292    Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp Asp Leu Thr Thr
293        130             135             140
294    Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu
295    145             150             155             160
296    Ala Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg Thr
297                165             170             175
298    Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr Gly
299            180             185             190
300    Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Arg Phe Gly His
301            195             200             205
302    Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn Pro Gly Trp Lys
303        210             215             220
304    Gly Gln Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln
305    225             230             235             240
306    His Gly Phe Cys Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp
307                245             250             255
308    Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His
309            260             265             270
310    Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly
311        275             280             285
312    Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro
313        290             295             300
314    Cys Lys Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr
315    305             310             315             320
316    Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ile Glu Ile
317                325             330             335
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/783,931**

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Input Set : **A:\7326-122**
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```
L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:13 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:61 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:377 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:439 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:1204 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=14
L:1201 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1433 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:1510 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:1665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:1723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:1746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:1765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:1833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1891 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1943 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1966 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1968 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:1997 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:2075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
```

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L:2096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:2251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:2268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:2270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:2276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:2295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:2297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:2611 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=81
L:2645 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=82
L:2723 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=86
L:2762 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=87
L:2807 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=89
L:2852 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=91
L:2897 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=93
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